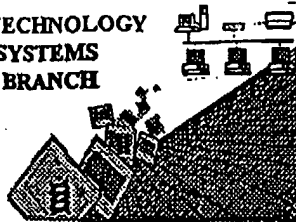BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US 09 487,841
Source: PTN16
Date Processed by STIC: 12-22-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

**ERROR DETECTED**   **SUGGESTED CORRECTION**   **SERIAL NUMBER:** 09/487,841

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
___ Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .5; this will
prevent "wrapping."

2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino   The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ___ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ___ Skipped Sequences   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8 ___ Skipped Sequences   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ___ Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

BEST AVAILABLE COPY
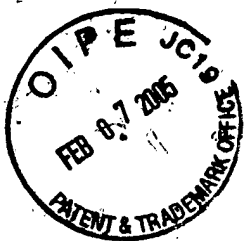
IFW16

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

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  4 <110> APPLICANT: Gravel, Roy A,
  5         Rozen, Rima
  6         Leclerc, Daniel
  7         Wilson, Aaron
  8         Rosenblatt, David
 10 <120> TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
 11         CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
 12         DEFECTS, CARDIOVASCULAR DISEASE, CANCER, AND DOWN'S SYNDROME
 15 <130> FILE REFERENCE: 50004/003004
 17 <140> CURRENT APPLICATION NUMBER: 09/487,841
 18 <141> CURRENT FILING DATE: 2000-01-19
 20 <150> PRIOR APPLICATION NUMBER: 09/371,347
 21 <151> PRIOR FILING DATE: 1999-08-10
 23 <150> PRIOR APPLICATION NUMBER: 09/232,028
 24 <151> PRIOR FILING DATE: 1999-01-15
 26 <150> PRIOR APPLICATION NUMBER: 60/071,622
 27 <151> PRIOR FILING DATE: 1998-01-16
 29 <160> NUMBER OF SEQ ID NOS: 61
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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Does Not Comply
Corrected Diskette Needed
(pg.3,5-19,12,14,16)

ERRORED SEQUENCES

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315 <210> SEQ ID NO: 21
316 <211> LENGTH: 698
317 <212> TYPE: PRT
318 <213> ORGANISM: Homo sapiens
320 <400> SEQUENCE: 21
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322 1               5               10              15
323 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
324             20              25              30
325 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
326         35              40              45
327 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
328     50              55              60
329 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
330 65              70              75              80
331 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
332             85              90              95
333 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
334             100             105             110
335 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
```

```
336           115                   120                   125
337 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
338      130             ·       135                   140
339 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
340 145                   150                   155                   160
341 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
342                   165     ·               170                   175
343 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
344            180                   185                   190
345 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
346            195                   200                   205
347 Gln Asn Ala Val Asn Ser·Asn Gln Ser Asn Val Val Ile Glu Asp Phe
348      210                   215                   220
349 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
350 225                   230                   235                   240
351 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu·Gln Val His Leu Gln Glu
352      '               245                   250             255·
353 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp·Pro
354            260                   265                   270
355 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
356      275                   280                   285     ·
357 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
358      290                   295             ·     300
359 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
360 305                   310                   315                   320
361 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
362                   325                   330                   335
363 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
364            340                   345                   350
365 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
366            355                   360·                  365
367 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
368      370                   375                   380     ·
369 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
370 385                   390                   395                   400
371 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
372                   405                   410                   415
373 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
374            420                   425                   430
375 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
376            435             ·     440                   445
377 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
378      450                   455             ·      460
379 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
380 465                   470                   475                   480
381 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
382 .                   485                   490                   495
383 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
384            500     ·               505                   510
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RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

          Input Set : A:\seqlist.txt
          Output Set: N:\CRF4\12222004\I487841.raw

    385 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
    386   515   520   525
    387 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
    388   530   535   540
    389 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
    390 545   550   555   560
    391 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
    392   565   570   575
    393 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
    394   580   585   590
    395 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
    396   595   600   605
    397 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
    398   610   615   620
    399 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
    400 625   630   635   640
    401 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
    402   645   650   655
    403 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
    404   660   665   670
E--> 405
Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu   675   680
    407 <210> SEQ ID NO: 22
    408 <211> LENGTH: 682
    409 <212> TYPE: PRT
    410 <213> ORGANISM: Caenorhabditis elegans
    412 <400> SEQUENCE: 22
    413 Met Thr Asp Phe Leu Ile Ala Phe Gly Ser Gln Thr Gly Gln Ala Glu
    414 1   5   10   15
    415 Thr Ile Ala Lys Ser Leu Lys Glu Lys Ala Glu Leu Ile Gly Leu Thr
    416   20   25   30
    417 Pro Arg Leu His Ala Leu Asp Glu Asn Glu Lys Lys Phe Asn Leu Asn
    418   35   40   45
    419 Glu Glu Lys Leu Cys Ala Ile Val Val Ser Ser Thr Gly Asp Gly Asp
    420   50   55   60
    421 Ala Pro Asp Asn Cys Ala Arg Phe Val Arg Arg Ile Asn Arg Asn Ser
    422 65   70   75   80
    423 Leu Glu Asn Glu Tyr Leu Lys Asn Leu Asp Tyr Val Leu Leu Gly Leu
    424   85   90   95
    425 Gly Asp Ser Asn Tyr Ser Ser Tyr Gln Thr Ile Pro Arg Lys Ile Asp
    426   100   105   110
    427 Lys Gln Leu Thr Ala Leu Gly Ala Asn Arg Leu Phe Asp Arg Ala Glu
    428   115   120   125
    429 Ala Asp Asp Gln Val Gly Leu Glu Leu Glu Val Glu Pro Trp Ile Glu
    430   130   135   140
    431 Lys Phe Phe Ala Thr Leu Ala Ser Arg Phe Asp Ile Ser Ala Asp Lys
    432 145   150   155   160
    433 Met Asn Ala Ile Thr Glu Ser Ser Asn Leu Lys Leu Asn Gln Val Lys
    434   165   170   175
    435 Thr Glu Glu Glu Lys Lys Ala Leu Leu Gln Lys Arg Ile Glu Asp Glu

(handwritten margin notes:) -See item # 1 on error summary p sheet, This is a global error throughout sequence.

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RAW SEQUENCE LISTING               DATE: 12/22/2004
PATENT APPLICATION:  US/09/487,841    TIME: 15:09:45

          Input Set : A:\seqlist.txt
          Output Set: N:\CRF4\12222004\I487841.raw

436            180                185                190
437 Glu Ser Asp Asp Glu Gly Arg Gly Arg Val Ile Gly Ile Asp Met Leu
438        195                200                205
439 Ile Pro Glu His Tyr Asp Tyr Pro Glu Ile Ser Leu Leu Lys Gly Ser
440        210                215                220
441 Gln Thr Leu Ser Asn Asp Glu Asn Leu Arg Val Pro Ile Ala Pro Gln
442 225                230                235                240
443 Pro Phe Ile Val Ser Ser Val Ser Asn Arg Lys Leu Pro Glu Asp Thr
444            245                250                255
445 Lys Leu Glu Trp Gln Asn Leu Cys Lys Met Pro Gly Val Val Thr Lys
446        260                265                270
447 Pro Phe Glu Val Leu Val Val Ser Ala Glu Phe Val Thr Asp Pro Phe
448        275                280                285
449 Ser Lys Lys Ile Lys Thr Lys Arg Met Ile Thr Val Asp Phe Gly Asp
450        290                295                300
451 His Ala Ala Glu Leu Gln Tyr Glu Pro Gly Asp Ala Ile Tyr Phe Cys
452 305                310                315                320
453 Val Pro Asn Pro Ala Leu Glu Val Asn Phe Ile Leu Lys Arg Cys Gly
454            325                330                335
455 Val Leu Asp Ile Ala Asp Gln Gln Cys Glu Leu Ser Ile Asn Pro Lys
456            340                345                350
457 Thr Glu Lys Ile Asn Ala Gln Ile Pro Gly His Val His Lys Ile Thr
458        355                360                365
459 Thr Leu Arg His Met Phe Thr Thr Cys Leu Asp Ile Arg Arg Ala Pro
460        370                375                380
461 Gly Arg Pro Leu Ile Arg Val Leu Ala Glu Ser Thr Ser Asp Pro Asn
462 385                390                395                400
463 Glu Lys Arg Arg Leu Leu Glu Leu Cys Ser Ala Gln Gly Met Lys Asp
464            405                410                415
465 Phe Thr Asp Phe Val Arg Thr Pro Gly Leu Ser Leu Ala Asp Met Leu
466            420                425                430
467 Phe Ala Phe Pro Asn Val Lys Pro Pro Val Asp Arg Leu Ile Glu Leu
468        435                440                445
469 Leu Pro Arg Leu Ile Pro Arg Pro Tyr Ser Met Ser Ser Tyr Glu Asn
470        450                455                460
471 Arg Lys Ala Arg Leu Ile Tyr Ser Glu Met Glu Phe Pro Ala Thr Asp
472 465                470                475                480
473 Gly Arg Arg His Ser Arg Lys Gly Leu Ala Thr Asp Trp Leu Asn Ser
474            485                490                495
475 Leu Arg Ile Gly Asp Lys Val Gln Val Leu Gly Lys Glu Pro Ala Arg
476            500                505                510
477 Phe Arg Leu Pro Pro Leu Gly Met Thr Lys Asn Ser Ala Gly Lys Leu
478        515                520                525
479 Pro Leu Leu Met Val Gly Pro Gly Thr Gly Val Ser Val Phe Leu Ser
480        530                535                540
481 Phe Leu His Phe Leu Arg Lys Leu Lys Gln Asp Ser Pro Ser Asp Phe
482 545                550                555                560
483 Val Asp Val Pro Arg Val Leu Phe Phe Gly Cys Arg Asp Ser Ser Val
484            565                570                575
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RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
    485 Asp Ala Ile Tyr Met Ser Glu Leu Glu Met Phe Val Ser Glu Gly Ile
    486             580             585             590
    487 Leu Thr Asp Leu Ile Ile Cys Glu Ser Glu Gln Lys Gly Glu Arg Val
    488             595             600     .           605
    489 Gln Asp Gly Leu Arg Lys Tyr Leu Asp Lys Val Leu Pro Phe Leu Thr.
    490     610             615             ·620    .
    491 Ala Ser Thr Glu Ser Lys Ile Phe Ile Cys Gly Asp Ala Lys Gly Met
    492 625             630             635             640
    493 Ser Lys Asp Val Trp Gln Cys Phe Ser Asp Ile Val Ala Ser Asp Gln
    494             645             650             655
E--> 495
Gly Ile Pro Asp Leu Glu Ala Lys Lys Lys Leu Met Asp Leu Lys Lys                660
    497 <210> SEQ ID NO: 23
    498 <211> LENGTH: 677
    499 <212> TYPE: PRT  .
    500 <213> ORGANISM: Homo sapiens
    502 <400> SEQUENCE: 23
E--> 503 Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val
    504 1               5               10              15
    505 Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser
    506             20              25              30
    507 Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys
    508             35              40              45
    509 Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val
    510     50              .   55              60
    511 Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile
    512 65              70              .   75              80
    513 Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn
    514             85              90              95
    515 Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala
    516             100             105             110
    517 Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile
    518             115             120  ·          125
    519 Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp
    520     130             135             140
    521 Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp
    522 145             150             155             160
    523 Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys
    524             165             170             175
    525 Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu
    526             180             .185            190
    527 Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp
    528             195             200             205
    529 Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp
    530     210             215             220
    531 Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser
    532 225             230             235             240
    533 Ser Ile Arg Gln Tyr Glu Leu·Val Val His Thr Asp Ile Asp Ala Ala
    534             245             250             255
    535 Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln
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RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
536              260              265              270
537 Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr
538         275              280              285
539 Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu
540     290              295              300
541 Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val
542 305              310              315              320
543 Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys
544             325              330              335
545 Ile Leu Gly Ala Asp Leu Asp Val Val Met Ser Leu Asn Asn Leu Asp
546         340              345              350
547 Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg
548         355              360              365
549 Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn
550     370              375              380
551 Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu
552 385              390              395              400
553 Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr
554             405              410              415
555 Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln
556         420              425              430
557 Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu
558         435              440              445
559 Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val
560     450              455              460
561 His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr
562 465              470              475              480
563 Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala
564             485              490              495
565 Lys Glu Pro Val Gly Glu Asn Gly Gly Arg Ala Leu Val Pro Met Phe
566         500              505              510
567 Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val
568     515              520              525
569 Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile
570     530              535              540
571 Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr
572 545              550              555              560
573 Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg
574             565              570              575
575 Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn
576         580              585              590
577 Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu
578     595              600              605
579 Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala
580     610              615              620
581 His Ile Tyr Val Cys Gly Asp Ala Arg Asn Met Ala Arg Asp Val Gln
582 625              630              635              640
583 Asn Thr Phe Tyr Asp Ile Val Ala Glu Leu Gly Ala Met Glu His Ala
E--> 584
        645              650              655     Gln Ala Val Asp Tyr Ile Lys Lys
```

```
   648 <210> SEQ ID NO: 25
   649 <211> LENGTH: 18
   650 <212> TYPE: PRT
   651 <213> ORGANISM: Homo sapiens
   653 <400> SEQUENCE: 25
E--> 654
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   656 <210> SEQ ID NO: 26
   657 <211> LENGTH: 18
   658 <212> TYPE: PRT
   659 <213> ORGANISM: Homo sapiens
   661 <400> SEQUENCE: 26
E--> 662
Gly Glu Thr Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr 1          5
   664 <210> SEQ ID NO: 27
   665 <211> LENGTH: 18
   666 <212> TYPE: PRT
   667 <213> ORGANISM: Oryctolagus cuniculus
   669 <400> SEQUENCE: 27
E--> 670
Gly Glu Thr Leu Leu Tyr Tyr Gly Cys Arg Arg Ala Ala Glu Asp Tyr 1          5
   672 <210> SEQ ID NO: 28
   673 <211> LENGTH: 18
   674 <212> TYPE: PRT
   675 <213> ORGANISM: Drosophila melanogaster
   677 <400> SEQUENCE: 28
E--> 678
Gly Glu Ser Ile Leu Tyr Phe Gly Cys Arg Lys Arg Ser Glu Asp Tyr 1          5
   680 <210> SEQ ID NO: 29
   681 <211> LENGTH: 18
   682 <212> TYPE: PRT
   683 <213> ORGANISM: Vigna radiata
   685 <400> SEQUENCE: 29
E--> 686
Gly Pro Ala Leu Leu Phe Phe Gly Cys Arg Asn Arg Gln Met Asp Phe 1          5
   688 <210> SEQ ID NO: 30
   689 <211> LENGTH: 18
   690 <212> TYPE: PRT
   691 <213> ORGANISM: Aspergillus niger
   693 <400> SEQUENCE: 30
E--> 694
Gly Pro Thr Val Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe 1          5
   696 <210> SEQ ID NO: 31
   697 <211> LENGTH: 18
   698 <212> TYPE: PRT
   699 <213> ORGANISM: Homo sapiens
   701 <400> SEQUENCE: 31
E--> 702
Cys Pro Met Val Leu Val Phe Gly Cys Arg Gln Ser Lys Ile Asp His 1          5
   704 <210> SEQ ID NO: 32
   705 <211> LENGTH: 18
   706 <212> TYPE: PRT
   707 <213> ORGANISM: Homo sapiens
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[Handwritten annotations: "✓ SAME errors", "See item # 1 on error Summary sheet."]

```
      709 <400> SEQUENCE: 32
E--> 710
Gly Arg Met Thr Leu Val Phe Gly Cys Arg Arg Pro Asp Glu Asp His 1                    5
      712 <210> SEQ ID NO: 33
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Same error

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841 TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
      713 <211> LENGTH: 18
      714 <212> TYPE: PRT
      715 <213> ORGANISM: Homo sapiens
      717 <400> SEQUENCE: 33
E--> 718
Thr Pro Met Thr Leu Val Phe Gly Cys Arg Cys Ser Gln Leu Asp His 1
      720 <210> SEQ ID NO: 34
      721 <211> LENGTH: 18
      722 <212> TYPE: PRT
      723 <213> ORGANISM: Oryctolagus cuniculus
      725 <400> SEQUENCE: 34
E--> 726
Gly Arg Met Thr Leu Val Phe Gly Cys Arg His Pro Glu Glu Asp His 1
      728 <210> SEQ ID NO: 35
      729 <211> LENGTH: 18
      730 <212> TYPE: PRT
      731 <213> ORGANISM: Gallus gallus
      733 <400> SEQUENCE: 35
E--> 734
Gly Asp Met Ile Leu Leu Phe Gly Cys Arg His Pro Asp Met Asp His 1
      736 <210> SEQ ID NO: 36
      737 <211> LENGTH: 18
      738 <212> TYPE: PRT
      739 <213> ORGANISM: Escherichia coli
      741 <400> SEQUENCE: 36
E--> 742
Gly Lys Asn Trp Leu Phe Phe Gly Asn Pro His Phe Thr Glu Asp Phe 1
      744 <210> SEQ ID NO: 37
      745 <211> LENGTH: 18
      746 <212> TYPE: PRT
      747 <213> ORGANISM: Saccharomyces cerevisiae
      749 <400> SEQUENCE: 37
E--> 750
Gly Glu Val Phe Leu Tyr Leu Gly Ser Arg His Lys Arg Glu Glu Tyr 1
      752 <210> SEQ ID NO: 38
      753 <211> LENGTH: 18
      754 <212> TYPE: PRT
      755 <213> ORGANISM: Thiocapsa roseopersicina
      757 <400> SEQUENCE: 38
E--> 758
Gly Arg Asn Trp Leu Ile Phe Gly Asn Arg His Phe His Arg Asp Phe 1
      760 <210> SEQ ID NO: 39
      761 <211> LENGTH: 19
      762 <212> TYPE: PRT
      763 <213> ORGANISM: Pisum sativum
      765 <400> SEQUENCE: 39
E--> 766
Gly Leu Ala Trp Leu Phe Leu Gly Val Ala Asn Val Asp Ser Leu Leu 1
      768 <210> SEQ ID NO: 40
      769 <211> LENGTH: 18
      770 <212> TYPE: PRT
      771 <213> ORGANISM: Spinacia oleracea
      773 <400> SEQUENCE: 40
```

(handwritten annotations in right margin: "✓ Same errors", "5 See item #", "1 on = error summary sheet", with "5" marks beside several entries)

E--> 774
Gly Leu Ala Trp Leu Phe Leu Gly Val Pro Thr Ser Ser Ser Leu Leu 1   *Same*   5
    818 <210> SEQ ID NO: 42   *error*
    819 <211> LENGTH: 698

```
820 <212> TYPE: PRT
821 <213> ORGANISM: Homo sapiens
823 <400> SEQUENCE: 42
824 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
825 1               5                   10                  15
826 Ala Ile Ala Glu Glu Ile Cys Glu Gln Ala Val Val His Gly Phe Ser
827             20                  25                  30
828 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
829         35                  40                  45
830 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
831     50                  55                  60
832 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
833 65                  70                  75                  80
834 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
835                 85                  90                  95
836 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
837             100                 105                 110
838 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
839         115                 120                 125
840 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
841     130                 135                 140
842 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
843 145                 150                 155                 160
844 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
845                 165                 170                 175
846 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
847             180                 185                 190
848 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
849         195                 200                 205
850 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
851     210                 215                 220
852 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
853 225                 230                 235                 240
854 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
855             245                 250                 255
856 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
857         260                 265                 270
858 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
859     275                 280                 285
860 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
861     290                 295                 300
862 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
863 305             310                 315                 320
864 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
865             325                 330                 335
866 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
867         340                 345                 350
868 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
869         355                 360                 365
```

```
870 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
871     370                 375                 380
872 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
873 385             390                 395                 400
874 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
875             405                 410                 415
876 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
877             420                 425                 430
878 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
879             435                 440                 445
880 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
881     450                 455                 460
882 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
883 465                 470                 475                 480
884 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
885             485                 490                 495
886 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
887             500                 505                 510
888 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
889             515                 520                 525
890 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
891     530                 535                 540
892 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
893 545                 550                 555                 560
894 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
895             565                 570                 575
896 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
897             580                 585                 590
898 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
899             595                 600                 605
900 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
901     610                 615                 620
902 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
903 625                 630                 635                 640
904 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
905             645                 650                 655
906 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
907             660                 665                 670
E--> 908
Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu    675                 680
952 <210> SEQ ID NO: 44
953 <211> LENGTH: 698
954 <212> TYPE: PRT
955 <213> ORGANISM: Homo sapiens
957 <400> SEQUENCE: 44
958 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
959 1               5                   10                  15
960 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
961             20                  25                  30
962 Ala Asp Leu His Thr Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
```

```
963        35                    40                    45
964 Glu Thr Ala Pro Leu Val Val Val Val Ser Thr Thr Gly Thr Gly Asp
965        50                    55                    60
966 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
967 65                    70                    75                    80
968 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
969                   85                    90                    95
970 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
971                   100                   105                   110
972 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
973             115                   120                   125
974 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
975       130                   135                   140
976 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
977 145                   150                   155                   160
978 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
979                   165                   170                   175
980 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
981             180                   185                   190
982 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
983             195                   200                   205
984 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
985       210                   215                   220
986 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
987 225                   230                   235                   240
988 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
989                   245                   250                   255
990 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
991             260                   265                   270
992 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
993       275                   280                   285
994 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
995       290                   295                   300
996 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
997 305                   310                   315                   320
998 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
999                   325                   330                   335
1000 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
1001             340                   345                   350
1002 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
1003             355                   360                   365
1004 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
1005       370                   375                   380
1006 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
1007 385                   390                   395                   400
1008 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
1009             405                   410                   415
1010 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
1011             420                   425                   430
```

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                    RAW SEQUENCE LISTING              DATE: 12/22/2004
                    PATENT APPLICATION:  US/09/487,841    TIME: 15:09:45

                    Input Set : A:\seqlist.txt
                    Output Set: N:\CRF4\12222004\I487841.raw

     1012 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
     1013         435             440                 445
     1014 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
     1015     450             455                 460
     1016 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
     1017 465             470                 475                 480
     1018 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
     1019             485                 490                 495
     1020 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
     1021         500                 505                 510
     1022 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
     1023         515                 520                 525
     1024 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
     1025     530             535                 540
     1026 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
     1027 545             550                 555                 560
     1028 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
     1029             565                 570                 575
     1030 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
     1031         580                 585                 590
     1032 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
     1033         595                 600                 605
     1034 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
     1035     610             615                 620
     1036 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
     1037 625             630                 635                 640
     1038 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
     1039             645                 650                 655
     1040 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
     1041             660                 665                 670
E--> 1042
Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu          675                   680
     1086 <210> SEQ ID NO: 46
     1087 <211> LENGTH: 697
     1088 <212> TYPE: PRT
     1089 <213> ORGANISM: Homo sapiens
     1091 <400> SEQUENCE: 46
     1092 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
     1093 1               5                   10                  15
     1094 Ala Ile Ala Glu Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
     1095             20                  25                  30
     1096 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
     1097         35                  40                  45
     1098 Glu Thr Ala Pro Leu Val Val Val Val Ser Thr Thr Gly Thr Gly Asp
     1099     50                  55                  60
     1100 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
     1101 65              70                  75                  80
     1102 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
     1103             85                  90                  95
     1104 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
```

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
1105              100              105              110
1106 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
1107          115              120              125
1108 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
1109     130              135              140
1110 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
1111 145              150              155              160
1112 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
1113              165              170              175
1114 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
1115          180 .            185              190
1116 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
1117          195              200              205
1118 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
1119     210                   215                   220
1120 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
1121 225              230              235              240
1122 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
1123              245              250              255
1124 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
1125          260              265              270
1126 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
1127          275              280              285
1128 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
1129     290              295              300
1130 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
1131 305              310              315              320
1132 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
1133              325              330              335
1134 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
1135          340              345              350
1136 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
1137          355              360              365
1138 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
1139     370              375              380
1140 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
1141 385              390              395              400
1142 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
1143              405              410              415
1144 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
1145          420              425              430
1146 Ser Cys Gln Pro Pro Leu Ser Leu Leu Leu Glu His Leu Pro Lys Leu
1147          435              440              445
1148 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
1149     450              455              460
1150 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
1151 465              470              475              480
1152 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
1153              485              490              495
```

RAW SEQUENCE LISTING   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:45

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
1154 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
1155             500             505             510
1156 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
1157         515             520             525
1158 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
1159     530             535             540
1160 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
1161 545             550             555             560
1162 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Phe
1163             565             570             575
1164 Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu Leu
1165         580             585             590
1166 Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser Phe
1167         595             600             605
1168 Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr Val
1169     610             615             620
1170 Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu Leu
1171 625             630             635             640
1172 Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met Ala
1173             645             650             655
1174 Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val Gly
1175             660             665             670
E--> 1176
Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu Glu      675          680
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:46

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:21; Line(s) 405
Seq#:22; Line(s) 495
Seq#:23; Line(s) 584
Seq#:25; Line(s) 654
Seq#:26; Line(s) 662
Seq#:27; Line(s) 670
Seq#:28; Line(s) 678
Seq#:29; Line(s) 686
Seq#:30; Line(s) 694
Seq#:31; Line(s) 702
Seq#:32; Line(s) 710
Seq#:33; Line(s) 718
Seq#:34; Line(s) 726
Seq#:35; Line(s) 734
Seq#:36; Line(s) 742
Seq#:37; Line(s) 750
Seq#:38; Line(s) 758
Seq#:39; Line(s) 766
Seq#:40; Line(s) 774
Seq#:42; Line(s) 908
Seq#:44; Line(s) 1042
Seq#:46; Line(s) 1176

VERIFICATION SUMMARY   DATE: 12/22/2004
PATENT APPLICATION: US/09/487,841   TIME: 15:09:46

Input Set : A:\seqlist.txt
Output Set: N:\CRF4\12222004\I487841.raw

```
L:405  M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:21
L:495  M:252 E: No. of Seq. differs, <211> LENGTH:Input:682 Found:656 SEQ:22
L:584  M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:23
L:584  M:252 E: No. of Seq. differs, <211> LENGTH:Input:677 Found:656 SEQ:23
L:654  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:662  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:670  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:678  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:686  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:694  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:702  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:710  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:718  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:726  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:734  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:742  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:750  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:758  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:766  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:774  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:908  M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:42
L:1042 M:252 E: No. of Seq. differs, <211> LENGTH:Input:698 Found:672 SEQ:44
L:1176 M:252 E: No. of Seq. differs, <211> LENGTH:Input:697 Found:672 SEQ:46
```